



Genetic parameters studies on bacterial blight resistance genes introgressed segregating population in Rice

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ABSTRACT

An exploratory research was conducted to know genetic parameters and agronomical performance of three bacterial blight resistance genes introgressed segregating population of CB 174 R × IRBB 60, CB 87 R × IRBB 60 and TNAU CMS 2B × IRBB 60 in rice. Higher range of genotypic and phenotypic coefficient of variation (GCV and PCV) was found in CB 87 R × IRBB 60 for the trait of number of grains and leads to develop/selection superior genotypes significantly. For single plant yield, CB 174 R × IRBB 60 cross showed high heritability (83.89%) and (27.45%) genetic advance (%) suggesting that traits were primarily controlled by additive gene action and thus, leads to easy selection. Whereas, estimate of moderate heritability (56.09%) with high genetic advance (24.66%) was found in the cross of CB 87 R × IRBB 60 indicating that postponement of selection and for the cross of TNAU CMS 2B × IRBB 60 showed higher heritability with moderate level of genetic advance (67.36% and 11.84%), revealed that single plant yield was preponderantly governed by both additive and non-additive gene effects and selection may be rewarded.

Keywords: Genetic parameters; Rice bacterial blight; Rice blast; Yield components

1. INTRODUCTION

In India, rice is most important stable food crop and its productivity has become significant (Subbaiah et al., 2011). To meet the demands of rice consumption, 121.2 million tons of rice will be estimated by the year 2030, 129.6 million tons by 2040 and 137.3 million tons by 2050 (C.R.R.I. Annual Report 2012-13). Among the segregating generations F_2 generation is most crucial, where selection has to be done more critically. For any improvement of breeding programme, genetic variability is indispensable for that. Heritability provides very utile information of morphogenetic traits can be transferred to successive breeding cycle (Bello et al., 2012).

High heritability with genetic advance (%) of mean could be much more useful to predict the desirable genotype/progeny for yield and their component traits of yield (Singh et al., 2011). Wide range of variability in segregating population mainly depends upon the relative importance of how diverse genotypes used for hybridization programme and thus, uplift the selection process. The current study was intended to know the extent of genetic parameters for yield and yield component traits in bacterial blight genes introgressed segregating populations of rice.

2. MATERIALS AND METHODS

CB 87 R and CB 174 R are the restorer lines of released rice hybrids CORH 3 (TNAU CMS 2A / CB 87R) and TNAU rice hybrid CO RH 4 (COMS 23A / CB 174 R) respectively and TNAU CMS 2B is the maintainer line for TNAU CMS 2A used as recurrent parents. IRBB 60 is used as the donor parent for bacterial blight genes (*Xa21*, *xa5*, *xa13*).

The F_2 populations of three crosses were namely CB 174 R \times IRBB 60, CB 87 R \times IRBB 60 and TNAU CMS 2B \times IRBB 60 were raised at Department of Rice, Tamil Nadu Agricultural University, Coimbatore, during the year of 2012-2013. Single seedling / hill were planted after 20-25 days by spaced at distance of 20 \times 20 cm.

Data was recorded on single plant basis for plant height (cm), productive tillers per plant, panicle length (cm), filled grains per panicle, thousand grain weight (g) and single plant yield (g) of each population.

Genetic parameters such as genotypic and phenotypic variance and, phenotypic and genotypic co-efficient of variation were calculated by Johnson et al. (1955) were classified as per the method by Sivasubramanian and Menon (1973). Broad sense heritability was estimated by Lush (1940) and classified by Robinson et al., (1949). Mean genetic advance (%) was measured (Johnson et al., 1955) and categorized by Robinson (1949).

3. RESULTS AND DISCUSSIONS

The frequency distribution based on skewness and kurtosis, thus provides the magnitude gene action and trait controlling genes number (Figure 1, Figure 2, Figure 3) and variability parameters (Table 1, Table 2, Table 3) of six quantitative traits recorded for three F_2 crosses and character wise results were presented hereunder.

Plant height

Moderate level of GCV (14.83%) and PCV (15.61%) was found in CB 174 R × IRBB 60 and the low GCV and PCV (8.09% and 8.55%) was observed in TNAU CMS 2B × IRBB 60. High heritability was found in all the cross combination CB 174 R × IRBB 60 (90.24%), TNAU CMS 2B × IRBB 60 (89.41%) and CB 87R × IRBB 60 (73.72%). High and moderate genetic advance (%) was observed in CB 174 R × IRBB 60 (29.03%) and TNAU CMS 2B × IRBB 60 (15.76%) and CB 87R × IRBB 60 (15.26%), respectively. High heritability with genetic advance (%) estimates were noticed in CB 174 R × IRBB 60, suggesting that traits were primarily controlled by additive gene action and thus, leads to easy selection (Singh et al., 2005; Kishore et al., 2008; Anjaneyulu et al., 2010; Bekele et al., 2013; Kiani et al., 2013; shrivastava et al., 2015). TNAU CMS 2B × IRBB 60 and CB 87R × IRBB 60 crosses showed high heritability with moderate genetic advance (%) was explained by both additive and non-additive gene effects and selection will be postponed later generation (Swain et al., 2006; Tuwar et al., 2013)

Number of productive tillers

The trait ranged from 6-17 in CB 174 R × IRBB 60, 4-13 in CB 87R × IRBB 60 and 9-19 in TNAU CMS 2B × IRBB 60. PCV is more than the GCV was observed in all the three crosses, indicating influence of environment in this trait. All studied cross combinations of CB 87 R × IRBB 60 (52.05%), TNAU CMS 2B × IRBB 60 (49.09%) and CB 174 R × IRBB 60 (39.68%) exhibited moderate heritability. Higher magnitude of genetic advance (%) was recorded for all combinations CB 87 R × IRBB 60 (24.94%), TNAU CMS 2B × IRBB 60 (21.01%) and CB 174 R × IRBB 60 (20.23%). This report was clinched that selection might be effective at later generation and get supported with our results (Kishore et al., 2008; Mural et al., 2012).

Panicle length

Panicle length ranged from 19-27 cm in CB 174 R × IRBB 60, 12-26.5 cm in CB 87 R × IRBB 60 and 19-25.5 cm in TNAU CMS 2B × IRBB 60. Observed GCV and PCV were low in all three crosses. Moderate heritability joined with genetic advance (%) for the cross of CB 87 R × IRBB 60 (50.43% and 14.54%). This finding was clued that efficient selection could be on the basis of agronomical desirability. Cross combination of TNAU CMS 2B × IRBB 60 (53.07%, 7.47%) and CB 174 R × IRBB 60 (48.68%, 8.46%) had moderate heritability with low genetic advance (%) of mean. This finding was suggested that improvement of this trait might be difficult through simple selection (Sathya and Jabaraj, 2013; Mazid et al., 2013; Bitew, 2016).

Number of grains per panicle

Grains per panicle ranged from 50-140 in CB 87 R × IRBB 60, 89-151 in CB 174 R × IRBB 60 and 98-142 in TNAU CMS 2B × IRBB 60. High GCV was observed in CB 87 R × IRBB 60 (21.70%) and low in CB174R × IRBB60 (9.81%). On the other hand, higher value of PCV was noticed in CB 87 R × IRBB 60 (22.40%) and lower in TNAU CMS 2B × IRBB 60 (10.66%). Higher estimate of heritability coupled genetic advance (%) was ascertained in CB 87 R × IRBB 60 (93.85% and 43.30%) and TNAU CMS 2B × IRBB 60 (98.01% and 21.53%), suggesting that little influence of environment and favourable for accumulating

more additive genes (Prasad et al., 2001; Sankar et al., 2006; Singh et al., 2007). Whereas, moderate heritability joined with genetic advance (%) of mean was found for the cross of CB 174 R × IRBB 60 (53.62% and 14.80%), indicating that expression of their trait under control and selection will be in carried out in advanced breeding cycle based on their phenotypic performance.

Thousand grain weight

The greater amount of variability was found for all the crosses, like CB 87 R × IRBB 60 (11.20-25.60 g) > CB 174 R × IRBB 60 (17.10-27.00 g) > (19.00-24.00 g) TNAU CMS 2B × IRBB 60. Estimated GCV and PCV were ranged as high CB 174 R × IRBB 60 in (8.77% and 11.29%) and low (4.87% and 5.51%) in TNAU CMS 2B × IRBB 60. CB 87 R × IRBB 60 cross combination (57.08% and 12.29%) had moderate estimate of heritability and genetic advance (%) of mean, respectively and thus, traits are genetically controlled and selection could be effective when phenotypic performance of the progeny. Higher estimate (60.33% and 14.04%) of heritability and moderate level of genetic advance (%) was estimated in CB 174 R × IRBB 60, indicating that character completely controlled by additive gene effects (Tuwar et al., 2013). While, for the cross of TNAU CMS 2B × IRBB 60 had higher and low level of heritability and genetic advance (%) was observed (78.09% and 8.87%), respectively and thus, preponderance of non-additive gene effects and selection may not be effective for this cross and trait in early segregating generation (Sarwar et al., 2015).

Single plant yield

Wider range of genotypic and phenotypic coefficient of variation was noticed as high (15.98% and 21.34%) in CB 87 R × IRBB 60 and low (7% and 8.53%) in TNAU CMS 2B × IRBB 60. Higher estimate of heritability coupled with genetic advance (%) was observed (83.89% and 27.45%) in CB 174R × IRBB 60, suggesting that additive gene effects play major role and improvement of this trait can be done through hybridization followed by pedigree breeding (Sankar et al., 2006; Binse et al., 2009; Gyanendra et al., 2011; Ahmad et al., 2015). Moderate heritability accompanied with high genetic advance (%) of mean was found (56.09% and 24.66%) in CB 87 R × IRBB 60. Whereas, TNAU CMS 2B × IRBB 60 showed (67.36% and 11.84%) higher heritability and moderate level of genetic advance (%) indicating that trait was governed by both additive and non-additive control (Sathya and Jabaraj, 2013).

3. CONCLUSION

Genetic variability analysis provide the basic information for viewing genetic attributes of the population on which breeding methods are useful for further improvement of breeding programme. Estimate of Heritability allow for genetic properties which will be carried to the subsequent generations. Existing available information from this materials based on genetic advance as per cent of mean and heritability, used as a tool for better selection efficiency.

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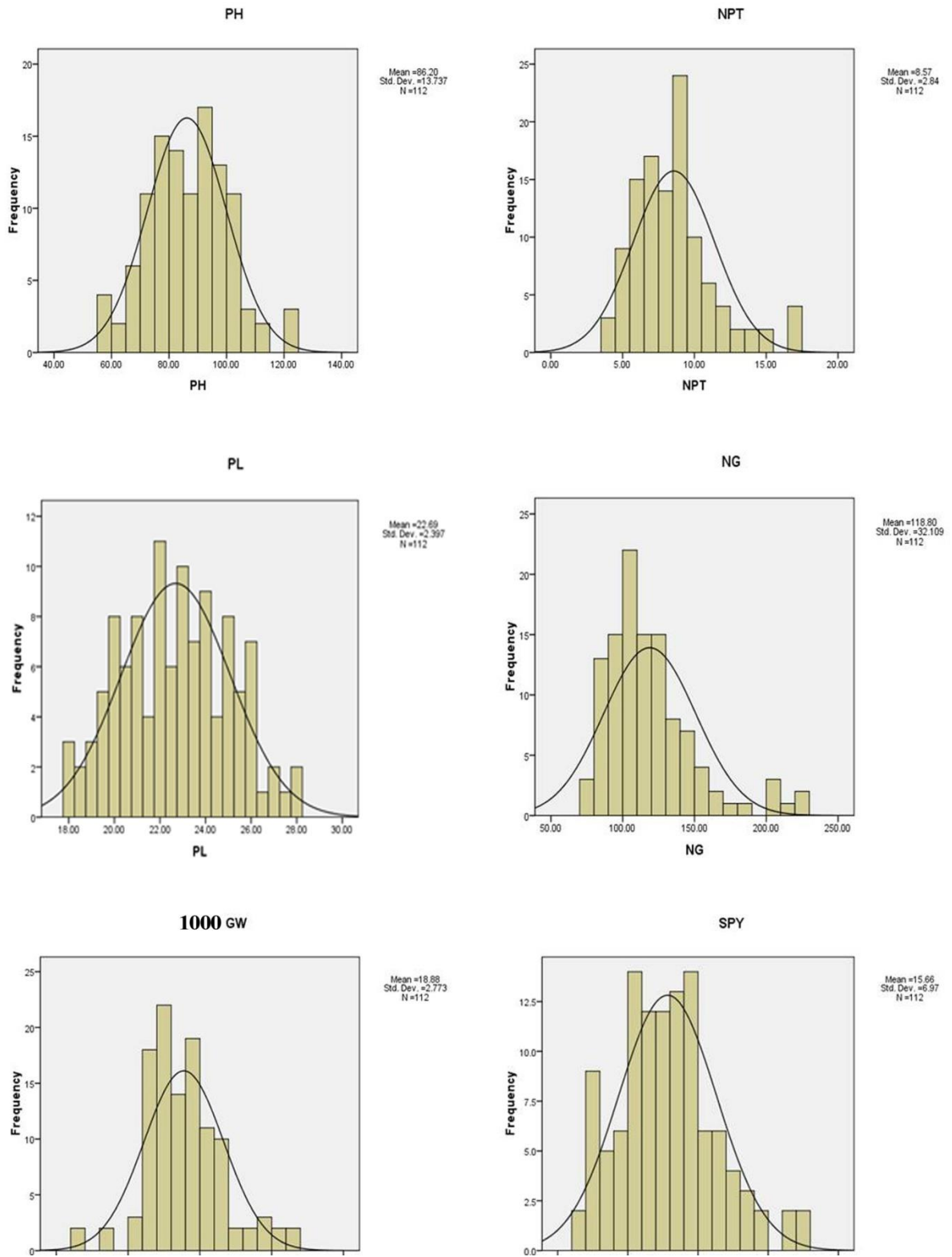


Figure 1. Frequency of distribution of Variability parameters in F₂ population of the cross CB 174R × IRBB 60 for yield and yield contributing traits in rice.

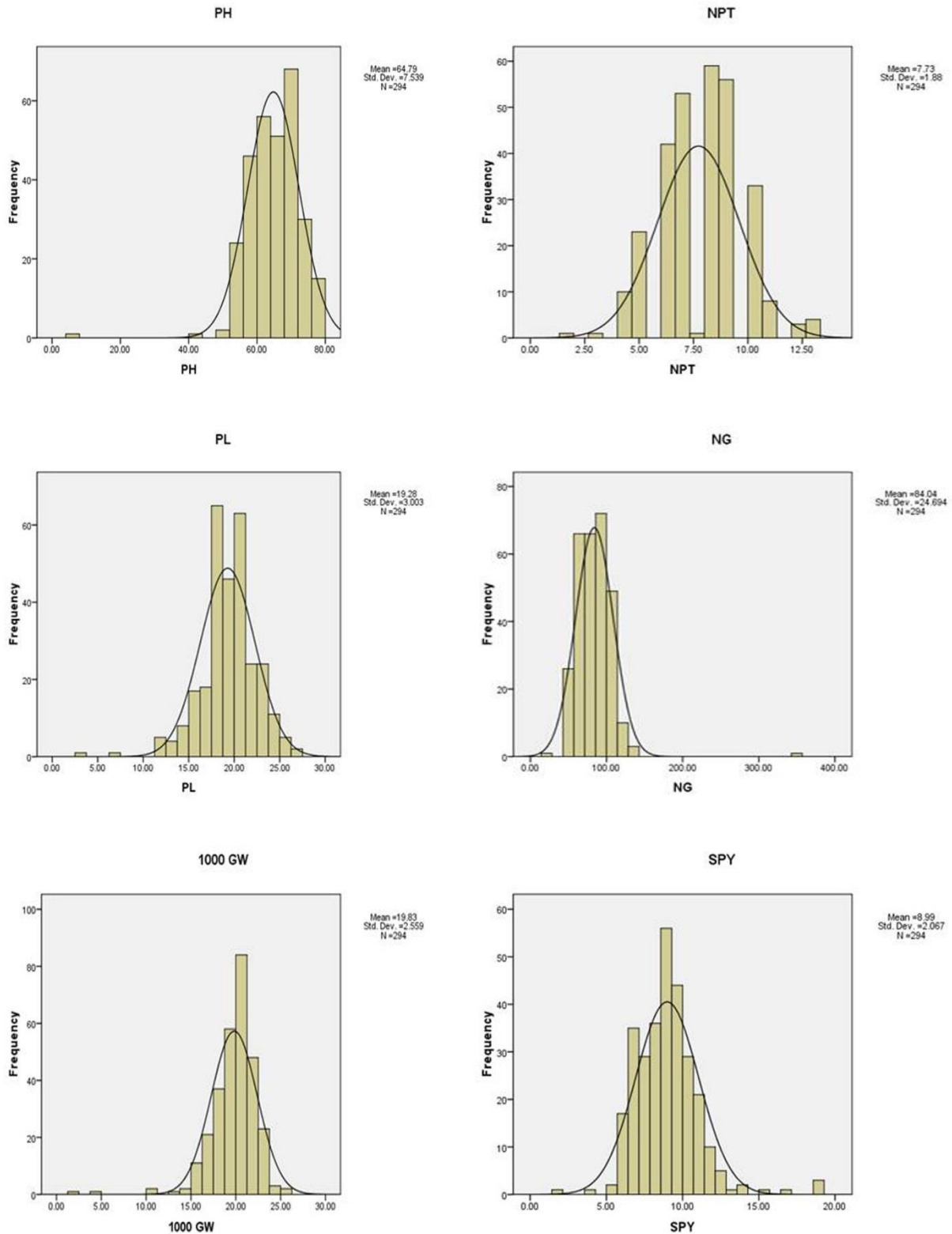


Figure 2. Frequency of distribution of Variability parameters in F₂ population of the cross CB 87 R × IRBB 60 for yield and yield contributing traits in rice.

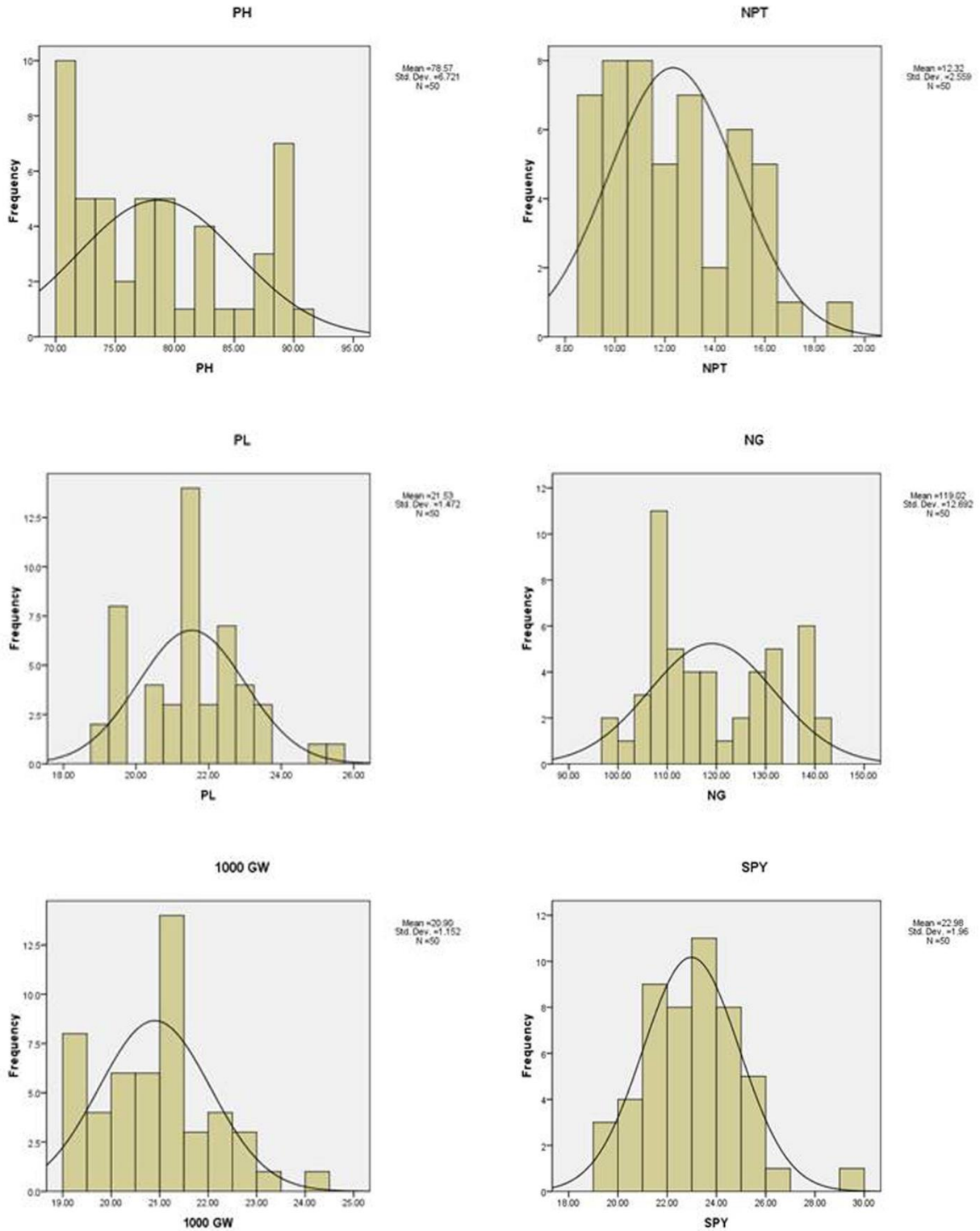


Figure 3. Frequency of distribution of Variability parameters in F₂ population of the cross TNAUCMS 2B × IRBB 60 for yield and yield contributing traits in rice.

Table 1. Variability parameters in F₂ population of the cross CB 174 R × IRBB 60 for yield and yield contributing traits in rice.

Characters	Range	Mean	GV (%)	PV (%)	GCV (%)	PCV (%)	Heritability (%)	GA of mean (%)
PH	79.00 – 135.50	100.44	221.94	245.94	14.83	15.61	90.24	29.03
NPT	6.00 – 17.00	10.54	2.69	6.8	15.59	24.75	39.68	20.23
PL	19.00 – 27.00	22.77	1.79	3.69	5.89	8.44	48.68	8.46
NG	89.00 – 151.00	118.73	135.79	253.25	9.81	13.4	53.62	14.8
1000GW	17.10 – 27.00	21.04	3.41	5.65	8.77	11.29	60.33	14.04
SPY	17.59 – 34.16	23.124	11.34	13.51	14.55	15.88	83.89	27.45

Note: PH: Plant height (cm), NPT: Number of productive tillers (nos), PL: Panicle length (cm), NG: Number of grains per panicle (nos), 1000GW: Thousand grain weight (g), SPY: Single plant yield (g).

Table 2. Variability parameters in F₂ population of the cross CB 87 R × IRBB 60 for yield and yield contributing traits in rice.

Characters	Range	Mean	GV (%)	PV (%)	GCV (%)	PCV (%)	Heritability (%)	GA of mean (%)
PH	49.00 – 78.50	65.07	31.52	42.75	8.63	10.05	73.72	15.26
NPT	4.00 – 13.00	8.68	1.69	3.26	16.78	23.26	52.05	24.94
PL	12.00 – 26.50	19.42	3.7	7.35	9.94	13.99	50.43	14.54
NG	50.00 – 140.00	83.28	326.63	348.04	21.7	22.4	93.85	43.3
1000GW	11.20 – 25.60	19.95	2.48	4.35	7.89	10.45	57.08	12.29
SPY	5.48 – 18.86	9.01	2.07	3.69	15.98	21.34	56.09	24.66

Note: PH: Plant height (cm), NPT: Number of productive tillers (nos), PL: Panicle length (cm), NG: Number of grains per panicle (nos), 1000GW: Thousand grain weight (g), SPY: Single plant yield (g).

Table 3. Variability parameters in F₂ population of the cross TNAU CMS 2B × IRBB 60 for yield and yield contributing traits in rice.

Characters	Range	Mean	GV (%)	PV (%)	GCV (%)	PCV (%)	Heritability (%)	GA of mean (%)
PH	70.00 – 90.00	78.57	40.39	45.17	8.09	8.55	89.41	15.76
NPT	9.00 – 19.00	12.32	3.21	6.55	14.55	20.77	49.09	21.01
PL	19.00 – 25.50	21.53	1.15	2.17	4.98	6.84	53.07	7.47
NG	98.00 – 142.00	119.02	157.87	161.08	10.56	10.66	98.01	21.53
1000GW	19.00 – 24.00	20.9	1.04	1.33	4.87	5.51	78.09	8.87
SPY	19.30 – 29.30	22.98	2.59	3.84	7.00	8.53	67.36	11.84

Note: PH: Plant height (cm), NPT: Number of productive tillers (nos), PL: Panicle length (cm), NG: Number of grains per panicle (nos), 1000GW: Thousand grain weight (g), SPY: Single plant yield (g).